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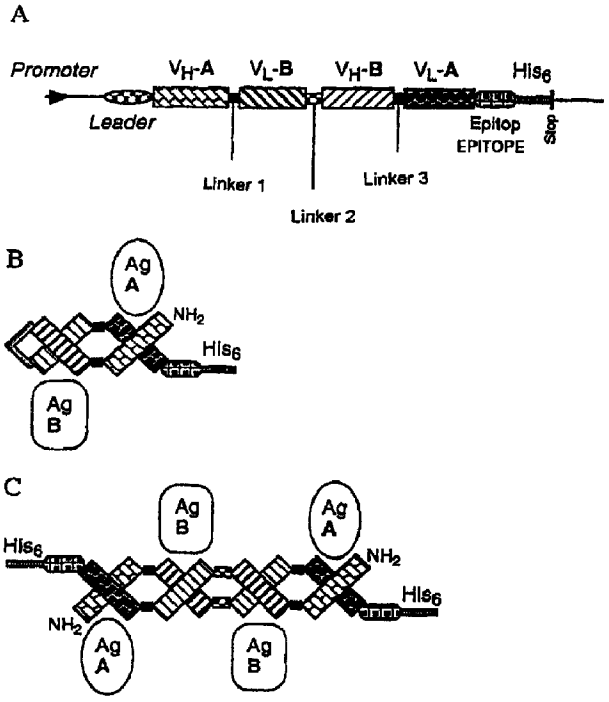
(54) **CONSTRUCTIONS D'ANTICORPS MULTIVALENTES**
(54) **MULTIVALENT ANTIBODY CONSTRUCTS**




(57) La présente invention concerne une construction d'anticorps $F_v$ multivalente, comportant au moins quatre domaines variables qui sont reliés l'un à l'autre par l'intermédiaire des segments peptidiques 1, 2 et 3. L'invention concerne en outre des plasmides d'expression qui codent pour une telle construction d'anticorps $F_v$, ainsi qu'un procédé de réalisation des constructions d'anticorps $F_v$ et leur utilisation.

(57) The invention relates to a multivalent $F_v$ antibody construct comprising at least four variable domains which are connected to one another via peptide linkers 1, 2 and 3. The invention also relates to expression plasmids which code for such an $F_v$ antibody construct. In addition, the invention relates to a method for producing the $F_v$ antibody constructs and to the use thereof.

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(54) Title: MULTIVALENT ANTIBODY CONSTRUCTS

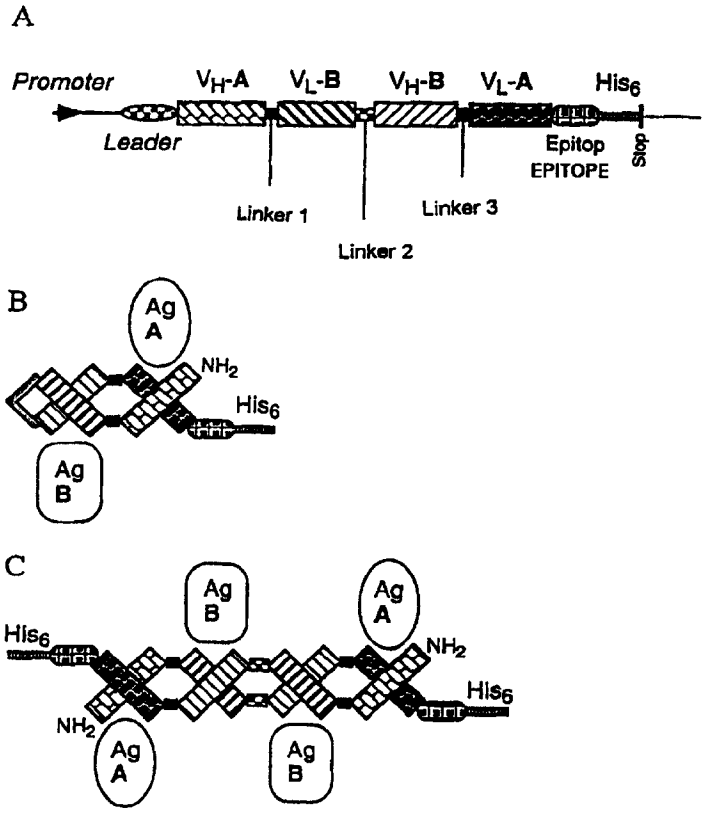
(54) Bezeichnung: MULTIVALENTE ANTIKÖRPER–KONSTRUKTE

(57) Abstract

The invention relates to a multivalent $F_v$ antibody construct comprising at least four variable domains which are connected to one another via peptide linkers 1, 2 and 3. The invention also relates to expression plasmids which code for such an $F_v$ antibody construct. In addition, the invention relates to a method for producing the $F_v$ antibody constructs and to the use thereof.

(57) Zusammenfassung

Die vorliegende Erfindung betrifft ein multivalentes $F_v$–Antikörper–Konstrukt mit mindestens vier variablen Domänen, die über die Peptidlinker 1, 2 und 3 miteinander verbunden sind. Ferner betrifft die Erfindung Expressionsplasmide, die für ein solches $F_v$–Antikörper–Konstrukt codieren, und ein Verfahren zur Herstellung der $F_v$–Antikörper–Konstrukte sowie deren Verwendung.



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# Multivalent Antibody Constructs

The present invention relates to multivalent $F_v$ antibody constructs, expression plasmids which code for them, and a method for producing the $F_v$ antibody constructs as well as the use thereof.

Natural antibodies are dimers and are therefore referred to as bivalent. They have four variable domains, namely two $V_H$ domains and two $V_L$ domains. The variable domains serve as binding sites for an antigen, a binding site being formed from a $V_H$ domain and a $V_L$ domain. Natural antibodies recognize one antigen each, so that they are also referred to as monospecific. Furthermore, they also have constant domains which add to the stability of the natural antibodies. On the other hand, they are also co-responsible for undesired immune responses which result when natural antibodies of various animal species are administered mutually.

In order to avoid such immune responses, antibodies are constructed which lack the constant domains. In particular, these are antibodies which only comprise the variable domains. Such antibodies are designated $F_v$ antibody constructs. They are often available in the form of single-chain monomers paired with one another.

However, it showed that $F_v$ antibody constructs only have little stability. Therefore, their usability for therapeutic purposes is strongly limited.

Thus, it is the object of the present invention to provide an antibody by means of which undesired immune responses can be avoided. Furthermore, it shall have a stability which makes it usable for therapeutic uses.

According to the invention this is achieved by the subject matters defined in the claims.

Therefore, the subject matter of the present invention relates to a multivalent $F_v$ antibody construct which has great stability. Such a construct is suitable for diagnostic and therapeutic purposes.

The present invention is based on the applicant's insights that the stability of an $F_v$ antibody construct can be increased if it is present in the form of a single-chain dimer where the four variable domains are linked with one another via three peptide linkers. The applicant also recognized that the $F_v$ antibody construct folds with itself when the middle peptide linker has a length of about 10 to 30 amino acids. The applicant also recognized that the $F_v$ antibody construct folds with other $F_v$ antibody constructs when the middle peptide linker has a length of about up to 10 amino acids so as to obtain a multimeric, i.e. multivalent, $F_v$ antibody construct. The applicant also realized that the $F_v$ antibody construct can be multi-specific.

According to the invention the applicant's insights are utilized to provide a multi-valent $F_v$ antibody construct

which comprises at least four variable domains which are linked with one another via peptide linkers 1, 2 and 3.

The expression "$F_v$ antibody construct" refers to an antibody which has variable domains but no constant domains.

The expression "multivalent $F_v$ antibody construct" refers to an $F_v$ antibody which has several, but at least four, variable domains. This is achieved when the single-chain $F_v$ antibody construct folds with itself so as to give four variable domains, or folds with other single-chain $F_v$ antibody constructs. In the latter case, an $F_v$ antibody construct is given which has 8, 12, 16, etc., variable domains. It is favorable for the $F_v$ antibody construct to have four or eight variable domains, i.e. it is bivalent or tetravalent (cf. Fig. 1). Furthermore, the variable domains may be equal or differ from one another, so that the antibody construct recognizes one or several antigens. The antibody construct preferably recognizes one or two antigens, i.e. it is monospecific and bispecific, respectively. Examples of such antigens are proteins CD19 and CD3.

The expression "peptide linkers 1, 3" refers to a peptide linker adapted to link variable domains of an $F_v$ antibody construct with one another. The peptide linker may contain any amino acids, the amino acids glycine (G), serine (S) and proline (P) being preferred. The peptide linkers 1 and 3 may be equal or differ from each other. Furthermore, the peptide linker may have a length of about 0 to 10 amino acids. In the former case, the peptide linker is only a peptide bond from the COOH residue of one of the variable domains and the $NH_2$ residue of another of the variable domains. The peptide linker preferably comprises the amino acid sequence GG.

The expression "peptide linker 2" refers to a peptide linker adapted to link variable domains of an $F_v$ antibody construct with one another. The peptide linker may contain any amino acids, the amino acids glycine (G), serine (S) and proline (P) being preferred. The peptide linker may also have a length of about 3 to 10 amino acids, in partiuclar 5 amino acids, and most particularly the amino acid sequence GGPGS, which serves for achieving that the single-chain $F_v$ antibody construct folds with other single-chain $F_v$ antibody constructs. The peptide linker can also have a length of about 11 to 20 amino acids, in particular 15 to 20 amino acids, and most particularly the amino acid sequence $(G_4S)_4$, which serves for achieving that the single-chain $F_v$ antibody construct folds with itself.

An $F_v$ antibody construct according to the invention can be produced by common methods. A method is favorable in which DNAs coding for the peptide linkers 1, 2 and 3 are ligated with DNAs coding for the four variable domains of an $F_v$ antibody construct such that the peptide linkers link the variable domains with one another and the resulting DNA molecule is expressed in an expression plasmid. Reference is made to Examples 1 to 6. As to the expressions "$F_v$ antibody construct" and "peptide linker" reference is made to the above explanations and, by way of supplement, to Maniatis, T. et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory 1982.

DNAs which code for an $F_v$ antibody construct according to the invention also represent a subject matter of the present invention. Furthermore, expression plasmids which contain such DNAs also represent a subject matter of the present invention. Preferred expression plasmids are pDISC3x19-LL,

pDISC3x19-SL, pPIC-DISC-LL, pPIC-DISC-SL, pDISC5-LL and pDISC6-SL. The first four were deposited with the DSMZ (*Deutsche Sammlung für Mikroorganismen und Zellen)* [German-type collection for micro-organisms and cells] on April 30, 1998 under DSM 12150, DSM 12149, DSM 12152 and DSM 12151, respectively.

Another subject matter of the present invention relates to a kit, comprising:

(a) an $F_v$ antibody construct according to the invention, and/or
(b) an expression plasmid according to the invention, and
(c) conventional auxiliary agents, such as buffers, solvents and controls.

One or several representatives of the individual components may be present.

The present invention provides a multivalent $F_v$ antibody construct where the variable domains are linked with one another via peptide linkers. Such an antibody construct distinguishes itself in that it contains no parts which can lead to undesired immune reactions. Furthermore, it has great stability. It also enables to bind several antigens simultaneously. Therefore, the $F_v$ antibody construct according to the invention is perfectly adapted to be used not only for diagnostic but also for therapeutic purposes. Such purposes can be seen as regards any disease, in particular a viral, bacterial or tumoral disease.

**Brief description of the drawings:**

**Fig. 1** shows the genetic organization of an $F_v$ antibody construct (A) according to the invention and schemes for forming a bivalent (B) or tetravalent $F_v$ antibody construct (C). Ag: antigen; $His_6$: six C-terminal histidine residues; stop: stop codon (TAA); $V_H$ and $V_L$: variable region of the heavy and light chains.

**Fig. 2** shows the scheme for the construction of the plasmids pDISC3x19-LL and pDISC3x19-SL. c-myc: sequence coding for an epitope which is recognized by the antibody 9E1, $His_6$: sequence which codes for six C-terminal histidine residues; PelB: signal peptide sequence of the bacterial pectate lyase (PelB leader); rbs: ribosome binding site; Stop: stop codon (TAA); $V_H$ and $V_L$: variable region of the heavy and light chains.

**Fig. 3** shows a diagram of the expression plasmid pDISC3x19-LL. 6xHis: sequence which codes for six C-terminal histidine residues; bla: gene which codes for ß-lactamase responsible for ampicillin resistance; bp: base pairs; c-myc: sequence coding for an epitope which is recognized by the 9E10 antibody; ColE1: origin of the DNA replication; f1-IG: intergenic region of the bacteriophage f1; Lac P/O: wt lac-operon promoter/operator; linker 1: sequence which codes for a GlyGly dipeptide linking the $V_H$ and $V_L$ domains; linker 2: sequence coding for a $(Gly_4Ser)_4$ polypeptide which links the hybrid scFv fragments; Pel-B leader: signal peptide sequence of the bacterial pectate lyase; rbs: ribosome binding site; $V_H$ and $V_L$: variable region of the heavy and light chains.

**Fig. 4** shows a diagram of the expression plasmid pDISC3x19-SL. 6xHis: sequence which codes for six C-terminal histidine

residues; bla: gene which codes for ß-lactamase which is responsible for the ampicillin resistance; bp: base pairs; c-myc: sequence coding for an epitope recognized by the 9E10 antibody; ColE1: origin of DNA replication; f1-IG: intergenic region of the bacteriophage f1; Lac P/O: wt lac-operon promoter/operator: linker 1: sequence which codes for a GlyGly dipeptide which links the $V_H$ and $V_L$ domains; linker 3: sequence which codes for a GlyGlyProGlySer oligopeptide which links the hybrid scFv fragments; Pel-B leader: signal peptide sequence of the bacterial pectate lyase; rbs: ribosome binding site; $V_H$ and $V_L$: variable region of the heavy and light chains.

**Fig. 5** shows the nucleotide sequence and the amino acid sequence derived therefrom of the bivalent $F_v$ antibody construct encoded by the expression plasmid pDIS3x19-LL. c-myc epitope: sequence coding for an epitope which is recognized by the antibody 9E10; CDR: region determining the complementarity; framework: framework region; His6 tail: sequence which codes for six C-terminal histidine residues; PelB leader: signal peptide sequence of the bacterial pectate lyase; RBS: ribosome binding site; $V_H$ and $V_L$: variable region of the heavy and light chains.

**Fig. 6** shows the nucleotide sequence and the derived amino acid sequence of the tetravalent $F_v$ antibody construct encoded by the expression plasmid pDISC3x19-SL. c-myc epitope: sequence coding for an epitope which is recognized by the 9E10 antibody; CDR: region determining complementarity; framework: framework region; His6 tail: sequence coding for the six C-terminal histidine residues; PelB leader: signal peptide sequence of the bacterial pectate lyase; RBS: ribosome binding site; $V_H$ and $V_L$: variable region of the heavy and light chains.

**Fig. 7** shows the nucleotide sequence and the derived amino acid sequence of a connection between a gene which codes for an α-factor leader sequence and a gene coding for the tetravalent $F_v$ antibody construct in the *Pichia* expression plasmid pPIC-DISC-SL. Alpha-factor signal: leader peptide sequence of the *Saccharomyces cerevisiae*-α factor secretion signal; $V_H$: variable region of the heavy chain. Rhombs indicate the signal cleaving sites.

**Fig. 8** shows the nucleotide sequence and the derived amino acid sequence of a connection between a gene coding for an α-factor leader sequence and a gene which codes for the bivalent $F_v$ antibody construct in the *Pichia* expression plasmid pPIC-DISC-LL. Alpha-factor signal: leader peptide sequence of the *Saccharomyces cerevisiae*-α factor secretion signal; $V_H$: variable region of the heavy chain. Rhombs show the signal cleaving sites.

**Fig. 9** shows a diagram of the expression plasmid pDISC5-LL. 6xHis: sequence coding for six C-terminal histidine residues; bla: gene which codes for ß-lactamase responsible for ampicillin resistance; bp: base pairs; c-myc: sequence coding for an epitope which is recognized by the 9E10 antibody; hok-sok: plasmid-stabilizing DNA locus; LacI: gene which codes for the Lac repressor; Lac P/O: wt lac-operon-promoter/operator; LacZ': gene which codes for the α-peptide of ß-galactosidase; linker 1: sequence which codes for a GlyGly dipeptide connecting the $V_H$ and $V_L$ domains; linker 2: sequence which codes for a $(Gly_4Ser)_4$ polypeptide linking the hybrid scFv fragments; M13 IG: intergenic region of the M13 bacteriophage; pBR322ori: origin of DNA replication; Pel-B leader: signal peptide sequence of the bacterial pectate lyase; rbs: ribosome binding site which originates

from the E. coli lacZ gene (lacZ), from the bacteriophage T7 gene 10 (T7g10) or from the *E. coli* skp gene (skp); skp: gene which codes for the bacterial periplasmic factor Skp/OmpH; tHP: strong transcription terminator; tIPP: transcription terminator; $V_H$ and $V_L$: variable region of the heavy and light chains.

**Fig. 10** shows a diagram of the expression plasmid pDISC6-SL. 6xHis: sequence which codes for six C-terminal histidine residues; bla: gene which codes for ß-lactamase responsible for ampicillin resistance; bp: base pairs: c-myc: sequence coding for an epitope which is recognized by the 9E10 antibody; hok-sok: plasmid-stabilized DNA locus; LacI: gene which codes for the Lac repressor; Lac P/O: wt lac-operon promoter/operator; LacZ': gene which codes for the α-peptide of ß-galactosidase; linker 1: sequence which codes for a GlyGly dipeptide which links the $V_H$ and $V_L$ domains; linker 3: sequence which codes for a GlyGlyProGlySer oligopeptide linking the hybrid scFv fragments: M13 IG: intergenic region of the M13 bacteriophage; pBR322ori: origin of DNA replication; Pel-B leader: signal peptide sequence of the bacterial pectate lyase; rbs: ribosome binding site originating from the *E. coli* lacZ gene (lacZ), from the bacteriophage T7 gene 10 (T7g10) or from the *E. coli* skp gene (skp); skp: gene which codes for the bacterial periplasmic factor Skp/OmpH; tHP: strong transcription terminator; tIPP: transcription terminator; $V_H$ and $V_L$: variable region of the heavy and light chains.

The invention is explained by the below examples.

**Example 1: Construction of the plasmids pDISC3x19-LL and pDISC3x19-SL for the expression of bivalent, bispecific and/or tetravalent, bispecific $F_v$ antibody constructs in bacteria**

The plasmids pHOG-αCD19 and pHOG-dmOKT3 which code for the scFv fragments derived from the hybridoma HD37 which is specific to human CD19 (Kipriyanov et al., 1996, J.-Immunol. Meth. 196, 51-62) and from the hybridoma OKT3 which is specific to human CD3 (Kipriyanov et al., 1997, Protein Eng. 10, 445-453), respectively, were used for the construction of expression plasmids for a single-chain $F_v$ antibody construct. A PCR fragment 1 of the $V_H$ domain of anti-CD19, followed by a segment which codes for a GlyGly linker, was produced using the primers DP1, 5'-TCACACAGAATTC-TTAGATCTATTAAAGAGGAGAAATTAACC, and DP2, 5'-AGCACACGATATCACCGCCAAGCTTGGGTGTTGTTTTGGC (cf. Fig. 2). The PCR fragment 1 was cleaved by EcoRI and EcoRV and ligated with the EcoRI/EcoRV-linearized plasmid pHOG-dmOKT3 so as to produce the vector pHOG19-3. The PCR fragment 2 of the $V_L$ domain of anti-CD19, followed by a segment which codes for a c-myc epitope and a hexahistidinyl tail, was produced using the primers DP3, 5'-AGCACACAAGCTTGGCGGTGATATCTTGCTCACCCAAAC-TCCA, and DP4, 5'-AGCACACTCTAGAGACACACAGATCTTTAGTGATGGTGAT-GGTGATGTGAGTTTAGG. The PCR fragment 2 was cleaved by HindIII and XbaI and ligated with the HIndIII/XbaI-linearized plasmid pHOG-dmOKT3 so as to obtain the vector pHOG3-19 (cf. Fig. 2). The gene coding for the hybrid scFv-3-19 in the plasmid pHOG3-19 was amplified by means of PCR with the primers Bi3sk, 5'-CAGCCGGCCATGGCGCAGGTGCAACTGCAGCAG and either Li-1, 5'-TATATACTGCAGCTGCACCTGGCTACCACCACCACCGGAGCCG-CCACCACCGCTACCACCGCCGCCAGAACCACCACCACCAGCGGCCGCAGCATCAGCCCG, for the production of a long flexible $(Gly_4Ser)_4$ inter-scFV linker (PCR fragment 3, cf. Fig. 2) or Li-2, 5'-TATATA-

CTGCAGCTGCACCTGCGACCCTGGGCCACCAGCGGCCGCAGCATCAGCCCG, for the production of a short rigid GGPGS linker (PCR fragment 4, cf. Fig. 2). The expression plasmids pDISC3x19-LL and pDISC3x19-SL were constructed by ligating the NcoI/PvuII restriction fragment from pHOG19-3, comprising the vector framework and the NcoI/PvuII-cleaved PCR fragments 3 and 4, respectively (cf. Figs. 3, 4). The complete nucleotide and protein sequences of the bivalent and tetravalent $F_v$ antibody constructs are indicated in Figs 5 and 6, respectively.

**Example 2: Construction of the plasmids pPIC-DISC-LL and pPIC-DISC-SL for the expression of bivalent, bispecific and/or tetravalent, bispecific $F_v$ antibody constructs in yeast**

(A) Construction of pPIC-DISC-SL

The vector pPICZαA (Invitrogen BV, Leek, Netherlands) for the expression and secretion of recombinant proteins in the yeast *Pichia pastoris* was used as a starting material. It contains a gene which codes for the *Saccharomyces cerevisiae* α-factor secretion signal, followed by a polylinker. The secretion of this vector is based on the dominant selectable marker, Zeocin™ which is bifunctional in both *Pichia* and *E. coli*. The gene which codes for the tetravalent $F_v$ antibody construct (scDia-SL) was amplified by means of PCR by the template pDISC3x19-SL using the primers 5-PIC, 5'-CCGTGAATTCCAGGTGCAACTGCAGCAGTCTGGGGCTGAACTGGC, and pSEXBn 5'-GGTCGACGTTAACCGACAAACAACAGATAAAACG. The resulting PCR product was cleaved by EcoRI and XbaI and ligated in EcoRI/XbaI-linearized pPICZαA. The expression plasmid pPIC-DISC-SL was obtained. The nucleotide and protein sequences

of the tetravalent $F_v$ antibody construct are shown in Fig. 7.

(B) Construction of pPIC-DISC-LL

The construction of pPIC-DISC-LL was carried out on the basis of pPICZαA (Invitrogen BV, Leek, Netherlands) and pDISC3x19-LL (cf. Fig. 3). The plasmid-DNA pPICZαA was cleaved by EcoRI. The overhanging 5'-ends were filled using a Klenow fragment of the *E. coli* DNA polymerase I. The resulting DNA was cleaved by XbaI, and the large fragment comprising the pPIC vector was isolated. Analogous thereto the DNA of pDISC3x19-LL was cleaved by NcoI and treated with a Klenow fragment. Following the cleavage using XbaI a small fragment, comprising a gene coding for the bivalent $F_v$ antibody, was isolated. Its ligation with a pPIC-derived vector-DNA resulted in the plasmid pPIC-DISC-LL. The nucleotide and protein sequences of the bivalent $F_v$ antibody construct are shown in Fig. 8.

**Example 3: Expression of the tetravalent and/or bivalent $F_v$ antibody construct in bacteria**

*E. coli* XL1-blue cells (Strategene, La Jolla, CA) which had been transformed with the expression plasmids pDISC3x19-LL and pDISC3x19-SL, respectively, were cultured overnight in 2xYT medium with 50 µg/ml ampicillin and 100 mM glucose ($2xYT_{Ga}$) at 37°C. 1:50 dilutions of the overnight cultures in $2xYT_{GA}$ were cultured as flask cultures at 37°C while shaking with 200 rpm. When the cultures had reached an $OD_{600}$ value of 0.8, the bacteria were pelleted by 10-minute centrifugation with 1500 g at 20°C and resuspended in the same volume of a fresh 2xYT medium containing 50 µg/ml ampicillin and 0.4 M saccharose. IPTG was added up to a

final concentration of 0.1 mM, and the growth was continued at room temperature (20-22°C) for 18 - 20 h. The cells were harvested by 10-minute centrifugation with 5000 g at 4°C. The culture supernatant was held back and stored on ice. In order to isolate the soluble periplasmic proteins, the pelleted bacteria were resuspended in 5 % of the initial volume of ice-cold 50 mM Tris-HCl, 20 % saccharose, 1 mM EDTA, pH 8.0. Following 1 hour of incubation on ice with occasional stirring the spheroplasts were centrifuged with 30,000 g at 4°C for 30 minutes, the soluble periplasmic extract being obtained as supernatant and the spheroplasts with the insoluble periplasmic material being obtained as pellet. The culture supernatant and the soluble periplasmic extract were combined and clarified by further centrifugation (30,000 g, 4°C, 40 min.). The recombinant product was concentrated by ammonium sulfate precipitation (final concentration 70 % saturation). The protein precipitate was obtained by centrifugation (10,000 g, 4°C, 40 min.) and dissolved in 10 % of the initial volume of 50 mM Tris-HCl, 1 M NaCl, pH 7.0. An immobilized metal affinity chromatography (IMAC) was carried out at 4°C using a 5 ml column of chelating sepharose (Pharmacia) which was charged with $Cu^{2+}$ and had been equilibrated with 50 mM Tris-HCl, 1 M NaCl, pH 7.0 (starting buffer). The sample was loaded by passing it over the column. It was then washed with twenty column volumes of starting buffer, followed by starting buffer with 50 mM imidazole until the absorption at 280 nm of the effluent was at a minimum (about thirty column volumes). The absorbed material was eluted with 50 mM Tris-HCl, 1 M NaCl, 250 mM imidazole, pH 7.0.

The protein concentrations were determined with the Bradford dye binding test (1976, Anal. Biochem. 72, 248-254) using the Bio-Rad (Munich, Germany) protein assay kit. The

concentrations of the purified tetravalent and bivalent $F_v$ antibody constructs were determined from the $A_{280}$ values using the extinction coefficients $\varepsilon^{1mg/ml}$ = 1.96 and 1.93, respectively.

**Example 4: Expression of the tetravalent and/or bivalent antibody construct in the yeast *Pichia pastoris***

Competent *P. pastoris* GS155 cells (Invitrogen) were electroporated in the presence of 10 µg plasmid-DNA of pPIC-DISC-LL and pPIC-DISC-SL, respectively, which had been linearized with SacI. The transformants were selected for 3 days at 30°C on YPD plates containing 100 µg/ml Zeocin™. The clones which secreted the bivalent and/or tetravalent $F_v$ antibody constructs were selected by plate screening using an anti-c-myc-mAk 9E10 (IC Chemikalien, Ismaning, Germany).

For the expression of the bivalent $F_v$ antibody constructs and tetravalent $F_v$ antibody constructs, respectively, the clones were cultured in YPD medium in shaking flasks for 2 days at 30°C with stirring. The cells were centrifuged resuspended in the same volume of the medium containing methanol and incubated for another 3 days at 30°C with stirring. The supernatants were obtained after the centrifugation. The recombinant product was isolated by ammonium sulfate precipitation, followed by IMAC as described above.

**Example 5: Characterization of the tetravalent $F_v$ antibody construct and bivalent $F_v$ antibody construct, respectively,**

(A) Size exclusion chromatography

An analytical gel filtration of the $F_v$ antibody constructs was carried out in PBS using a superdex 200-HR10/30 column (Pharmacia). The sample volume and the flow rate were 200 µl/min and 0.5 ml/min, respectively. The column was calibrated with high-molecular and low-molecular gel filtration calibration kits (Pharmacia).

(B) Flow cytometry

The human $CD3^+/CD19^-$-acute T-cell leukemia line Jurkat and the $CD19^+/CD3^-$ B-cell line JOK-1 were used for flow cytometrie. 5 x $10^5$ cells in 50 µl RPMI 1640 medium (GIBCO BRL, Eggestein, Germany) which was supplemented with 10 % FCS and 0.1 % sodium azide (referred to as complete medium) were incubated with 100 µl of the $F_v$ antibody preparations for 45 minutes on ice. After washing using the complete medium the cells were incubated with 100 µl 10 µg/ml anti-c-myc-Mak 9E10 (IC Chemikalien) in the same buffer for 45 min on ice. After a second wash cycle, the cells were incubated with 100 µl of the FITC-labeled goat-anti-mouse-IgG (GIBCO BRL) under the same conditions as before. The cells were then washed again and resuspended in 100 µl 1 µg/ml propidium iodide solution (Sigma, Deisenhofen, Germany) in complete medium with the exclusion of dead cells. The relative fluorescence of the stained cells was measured using a FACScan flow cytometer (Becton Dickinson, Mountain View, CA).

(C) Cytotoxicity test

The CD19-expressing Burkitt lymphoma cell line Raji and Namalwa were used as target cells. The cells were incubated in RPMI 1640 (GIBCO BRL) which was supplemented with 10 %

heat-inactivated FCS (GIBCO BRL), 2 mM glutamine and 1 mM pyruvate, at 37°C in a dampened atmosphere with 7.5 % $CO_2$. The cytotoxic T-cell tests were carried out in RPMI-1640 medium supplemented with 10 % FCS, 10 mM HEPES, 2 mM glutamine, 1 mM pyruvate and 0.05 mM 2-ME. The cytotoxic activity was evaluated using a standard[$^{51}$Cr] release test; 2 x $10^6$ target cells were labeled with 200 µCi Na[$^{51}$Cr]$O_4$ (Amersham-Buchler, Braunschweig, Germany) and washed 4 times and then resuspended in medium in a concentration of 2 x $10^5$/ml. The effector cells were adjusted to a concentration of 5 x $10^6$/ml. Increasing amounts of CTLs in 100 µl were titrated to $10^4$ target cells/well or cavity in 50 µl. 50 µl antibodies were added to each well. The entire test was prepared three times and incubated at 37°C for 4 h. 100 µl of the supernatant were collected and tested for [$^{51}$Cr] release in a gamma counter (Cobra Auto Gamma; Canberra Packard, Dreieich, Germany). The maximum release was determined by incubation of the target cells in 10 % SDS, and the spontaneous release was determined by incubation of the cells in medium alone. The specific lysis (%) was calculated as: (experimental release - spontaneous release)/(maximum release - spontaneous release) x 100.

**Example 6: Construction of the plasmids pDISC5-LL and pDISC5-SL for the expression of bivalent, bispecific and/or tetravalent, bispecific $F_v$ antibody constructs in bacteria by high cell density fermentation**

Expression vectors were prepared which contained the hok/sok plasmid-free cell suicide system and a gene which codes for the Skp/OmpH periplasmic factor for a greater production of recombinant antibodies. The skp gene was amplified by PCR using the primers skp-1, 5'-CGA ATT CTT AAG ATA AGA AGG AGT

TTA TTG TGA AAA AGT GGT TAT TAG CTG CAG G and skp-2, 5'-CGA ATT AAG CTT CAT TAT TTA ACC TGT TTC AGT ACG TCG G using the plasmid pGAH317 (Holck and Kleppe, 1988, Gene 67, 117-124). The resulting PCR fragment was cleaved by AflII and HindIII and inserted in the AflII/HindIII-linearized plasmid pHKK (Horn et al., 1996, Appl. Microbiol. Biotechnol. 46, 524-532) so as to obtain the vector pSKK. The genes obtained in the plasmids pDISC3x19-LL and pDISC3x19-SL and coding for the scFv antibody constructs were amplified by means of the primers fe-1, 5'-CGA ATT TCT AGA TAA GAA GGA GAA ATT AAC CAT GAA ATA CC and fe-2, 5'-CGA ATT CTT AAG CTA TTA GTG ATG GTG ATG GTG ATG TGA G. The XbaI/AflII-cleaved PCR fragments were inserted in pSKK before the skp insert so as to obtain the expression plasmids pDISC5-LL and pDISC6-SL, respectively, which contain tri-cistronic operons under the control of the lac promoter/operator system (cf. figs. 9, 10).

SEQUENCE RECORD

(1) GENERAL INDICATIONS:
(i) APPLICANT:
(A) NAME: Deutsches Krebsforschungszentrum
(B) STREET: Im Neuenheimer Feld 280
(C) TOWN: Heidelberg
(E) COUNTRY: Germany
(F) POSTAL CODE: 69120
(ii) TITLE OF THE INVENTION: Multivalent Antibody Constructs
(iii) NUMBER OF SEQUENCES: 17
(iv) COMPUTER-READABLE VERSION:
(A) DATA CARRIER: floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, version #1.30 (EPA)

(2) INDICATIONS AS TO SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1698 base pairs
(B) KIND: nucleotide
(C) STRAND TYPE: single strand
(D) TOPOLOGY: linear
(ii) KIND OF MOLECULE: genome DNA
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(ix) FEATURE:
(A) NAME/KEY: CDS
(B) POSITION: 28..1689
(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) POSITION: 28..1689
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
GAATTCATTA AAGAGGAGAA ATTAACC ATG AAA TAC CTA TTG CCT ACG GCA          51
                              Met Lys Tyr Leu Leu Pro Thr Ala
                                1               5
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```
GCC GCT GGC TTG CTG CTG CTG GCA GCT CAG CCG GCC ATG GCG CAG GTG        99
Ala Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val
     10                  15                  20

CAA CTG CAG CAG TCT GGG GCT GAA CTG GCA AGA CCT GGG GCC TCA GTG       147
Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val
 25                  30                  35                  40

AAG ATG TCC TGC AAG GCT TCT GGC TAC ACC TTT ACT AGG TAC ACG ATG       195
Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met-
                 45                  50                  55

CAC TGG GTA AAA CAG AGG CCT GGA CAG GGT CTG GAA TGG ATT GGA TAC       243
His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
             60                  65                  70

ATT AAT CCT AGC CGT GGT TAT ACT AAT TAC AAT CAG AAG TTC AAG GAC       291
Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
         75                  80                  85

AAG GCC ACA TTG ACT ACA GAC AAA TCC TCC AGC ACA GCC TAC ATG CAA       339
Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
     90                  95                  100

CTG AGC AGC CTG ACA TCT GAG GAC TCT GCA GTC TAT TAC TGT GCA AGA       387
Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
105                 110                 115                 120

TAT TAT GAT GAT CAT TAC AGC CTT GAC TAC TGG GGC CAA GGC ACC ACT       435
Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr
                125                 130                 135

CTC ACA GTC TCC TCA GCC AAA ACA ACA CCC AAG CTT GGC GGT GAT ATC       483
Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile
            140                 145                 150

TTG CTC ACC CAA ACT CCA GCT TCT TTG GCT GTG TCT CTA GGG CAG AGG       531
Leu Leu Thr Gln Thr Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
        155                 160                 165

GCC ACC ATC TCC TGC AAG GCC AGC CAA AGT GTT GAT TAT GAT GGT GAT       579
Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp
    170                 175                 180

AGT TAT TTG AAC TGG TAC CAA CAG ATT CCA GGA CAG CCA CCC AAA CTC       627
Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu
185                 190                 195                 200

CTC ATC TAT GAT GCA TCC AAT CTA GTT TCT GGG ATC CCA CCC AGG TTT       675
Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe
                205                 210                 215

AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC CTC AAC ATC CAT CCT GTG       723
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val
            220                 225                 230
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GAG AAG GTG GAT GCT GCA ACC TAT CAC TGT CAG CAA AGT ACT GAG GAT      771
Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp
        235                 240                 245

CCG TGG ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGG GCT GAT      819
Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp
    250                 255                 260

GCT GCG GCC GCT GGT GGT GGT GGT TCT GGC GGC GGT GGT AGC GGT GGT      867
Ala Ala Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
265                 270                 275                 280

GGC GGC TCC GGT GGT GGT GGT AGC CAG GTG CAG CTG CAG CAG TCT GGG      915
Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly
                285                 290                 295

GCT GAG CTG GTG AGG CCT GGG TCC TCA GTG AAG ATT TCC TGC AAG GCT      963
Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala
            300                 305                 310

TCT GGC TAT GCA TTC AGT AGC TAC TGG ATG AAC TGG GTG AAG CAG AGG     1011
Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg
        315                 320                 325

CCT GGA CAG GGT CTT GAG TGG ATT GGA CAG ATT TGG CCT GGA GAT GGT     1059
Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly
    330                 335                 340

GAT ACT AAC TAC AAT GGA AAG TTC AAG GGT AAA GCC ACT CTG ACT GCA     1107
Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala
345                 350                 355                 360

GAC GAA TCC TCC AGC ACA GCC TAC ATG CAA CTC AGC AGC CTA GCA TCT     1155
Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser
                365                 370                 375

GAG GAC TCT GCG GTC TAT TTC TGT GCA AGA CGG GAG ACT ACG ACG GTA     1203
Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val
            380                 385                 390

GGC CGT TAT TAC TAT GCT ATG GAC TAC TGG GGT CAA GGA ACC TCA GTC     1251
Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
        395                 400                 405

ACC GTC TCC TCA GCC AAA ACA ACA CCC AAG CTT GGC GGT GAT ATC GTG     1299
Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Val
    410                 415                 420

CTC ACT CAG TCT CCA GCA ATC ATG TCT GCA TCT CCA GGG GAG AAG GTC     1347
Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val
425                 430                 435                 440

ACC ATG ACC TGC AGT GCC AGC TCA AGT GTA AGT TAC ATG AAC TGG TAC     1395
Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
                445                 450                 455
```

```
CAG CAG AAG TCA GGC ACC TCC CCC AAA AGA TGG ATT TAT GAC ACA TCC      1443
Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser
            460                 465                 470

AAA CTG GCT TCT GGA GTC CCT GCT CAC TTC AGG GGC AGT GGG TCT GGG      1491
Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly
        475                 480                 485

ACC TCT TAC TCT CTC ACA ATC AGC GGC ATG GAG GCT GAA GAT GCT GCC      1539
Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala
    490                 495                 500

ACT TAT TAC TGC CAG CAG TGG AGT AGT AAC CCA TTC ACG TTC GGC TCG      1587
Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser
505                 510                 515                 520

GGG ACA AAG TTG GAA ATA AAC CGG GCT GAT ACT GCA CCA ACT GGA TCC      1635
Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly Ser
                525                 530                 535

GAA CAA AAG CTG ATC TCA GAA GAA GAC CTA AAC TCA CAT CAC CAT CAC      1683
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His His
            540                 545                 550

CAT CAC TAATCTAGA                                                   1698
His His
```

(2) INDICATIONS AS TO ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 554 amino acids

(B) KIND: amino acid

(D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1               5                  10                  15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20                  25                  30

Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35                  40                  45

Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
    50                  55                  60

Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65                  70                  75                  80
```

Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
100 105 110

Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
130 135 140

Thr Pro Lys Leu Gly Gly Asp Ile Leu Leu Thr Gln Thr Pro Ala Ser
145 150 155 160

Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser
165 170 175

Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln
180 185 190

Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu
195 200 205

Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr
225 230 235 240

His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr
245 250 255

Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Ala Ala Gly Gly Gly Gly
260 265 270

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
275 280 285

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
290 295 300

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
305 310 315 320

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
325 330 335

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
340 345 350

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
355 360 365

```
Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
    370                 375                 380

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
385                 390                 395                 400

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr
                405                 410                 415

Pro Lys Leu Gly Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Met
            420                 425                 430

Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser
        435                 440                 445

Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro
    450                 455                 460

Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala
465                 470                 475                 480

His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
                485                 490                 495

Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
            500                 505                 510

Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg
        515                 520                 525

Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu
    530                 535                 540

Asp Leu Asn Ser His His His His His His
545                 550
```

(2) INDICATIONS AS TO ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1653 base pairs

(B) KIND: nucleotide

(C) STRAND TYPE: single strand

(D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: genome DNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) POSITION: 28..1644

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) POSITION: 28..1644
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
GAATTCATTA AAGAGGAGAA ATTAACC ATG AAA TAC CTA TTG CCT ACG GCA          51
                                Met Lys Tyr Leu Leu Pro Thr Ala
                                  1               5

GCC GCT GGC TTG CTG CTG CTG GCA GCT CAG CCG GCC ATG GCG CAG GTG          99
Ala Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val
     10                  15                  20

CAA CTG CAG CAG TCT GGG GCT GAA CTG GCA AGA CCT GGG GCC TCA GTG         147
Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val
 25                  30                  35                  40

AAG ATG TCC TGC AAG GCT TCT GGC TAC ACC TTT ACT AGG TAC ACG ATG         195
Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met
                 45                  50                  55

CAC TGG GTA AAA CAG AGG CCT GGA CAG GGT CTG GAA TGG ATT GGA TAC         243
His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
             60                  65                  70

ATT AAT CCT AGC CGT GGT TAT ACT AAT TAC AAT CAG AAG TTC AAG GAC         291
Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
         75                  80                  85

AAG GCC ACA TTG ACT ACA GAC AAA TCC TCC AGC ACA GCC TAC ATG CAA         339
Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
     90                  95                 100

CTG AGC AGC CTG ACA TCT GAG GAC TCT GCA GTC TAT TAC TGT GCA AGA         387
Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
105                 110                 115                 120

TAT TAT GAT GAT CAT TAC AGC CTT GAC TAC TGG GGC CAA GGC ACC ACT         435
Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr
                125                 130                 135

CTC ACA GTC TCC TCA GCC AAA ACA ACA CCC AAG CTT GGC GGT GAT ATC         483
Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile
            140                 145                 150

TTG CTC ACC CAA ACT CCA GCT TCT TTG GCT GTG TCT CTA GGG CAG AGG         531
Leu Leu Thr Gln Thr Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
        155                 160                 165

GCC ACC ATC TCC TGC AAG GCC AGC CAA AGT GTT GAT TAT GAT GGT GAT         579
Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp
    170                 175                 180
```

```
AGT TAT TTG AAC TGG TAC CAA CAG ATT CCA GGA CAG CCA CCC AAA CTC        627
Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu
185                 190                 195                 200

CTC ATC TAT GAT GCA TCC AAT CTA GTT TCT GGG ATC CCA CCC AGG TTT        675
Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe
                205                 210                 215

AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC CTC AAC ATC CAT CCT GTG        723
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val
            220                 225                 230

GAG AAG GTG GAT GCT GCA ACC TAT CAC TGT CAG CAA AGT ACT GAG GAT        771
Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp
        235                 240                 245

CCG TGG ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGG GCT GAT        819
Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp
    250                 255                 260

GCT GCG GCC GCT GGT GGC CCA GGG TCG CAG GTG CAG CTG CAG CAG TCT        867
Ala Ala Ala Ala Gly Gly Pro Gly Ser Gln Val Gln Leu Gln Gln Ser
265                 270                 275                 280

GGG GCT GAG CTG GTG AGG CCT GGG TCC TCA GTG AAG ATT TCC TGC AAG        915
Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
                285                 290                 295

GCT TCT GGC TAT GCA TTC AGT AGC TAC TGG ATG AAC TGG GTG AAG CAG        963
Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
            300                 305                 310

AGG CCT GGA CAG GGT CTT GAG TGG ATT GGA CAG ATT TGG CCT GGA GAT       1011
Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
        315                 320                 325

GGT GAT ACT AAC TAC AAT GGA AAG TTC AAG GGT AAA GCC ACT CTG ACT       1059
Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
    330                 335                 340

GCA GAC GAA TCC TCC AGC ACA GCC TAC ATG CAA CTC AGC AGC CTA GCA       1107
Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
345                 350                 355                 360

TCT GAG GAC TCT GCG GTC TAT TTC TGT GCA AGA CGG GAG ACT ACG ACG       1155
Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
                365                 370                 375

GTA GGC CGT TAT TAC TAT GCT ATG GAC TAC TGG GGT CAA GGA ACC TCA       1203
Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
            380                 385                 390

GTC ACC GTC TCC TCA GCC AAA ACA ACA CCC AAG CTT GGC GGT GAT ATC       1251
Val Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile
        395                 400                 405
```

```
GTG CTC ACT CAG TCT CCA GCA ATC ATG TCT GCA TCT CCA GGG GAG AAG      1299
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
    410                 415                 420

GTC ACC ATG ACC TGC AGT GCC AGC TCA AGT GTA AGT TAC ATG AAC TGG      1347
Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
425                 430                 435                 440

TAC CAG CAG AAG TCA GGC ACC TCC CCC AAA AGA TGG ATT TAT GAC ACA      1395
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
                445                 450                 455

TCC AAA CTG GCT TCT GGA GTC CCT GCT CAC TTC AGG GGC AGT GGG TCT      1443
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
            460                 465                 470

GGG ACC TCT TAC TCT CTC ACA ATC AGC GGC ATG GAG GCT GAA GAT GCT      1491
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
        475                 480                 485

GCC ACT TAT TAC TGC CAG CAG TGG AGT AGT AAC CCA TTC ACG TTC GGC      1539
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
    490                 495                 500

TCG GGG ACA AAG TTG GAA ATA AAC CGG GCT GAT ACT GCA CCA ACT GGA      1587
Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly
505                 510                 515                 520

TCC GAA CAA AAG CTG ATC TCA GAA GAA GAC CTA AAC TCA CAT CAC CAT      1635
Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His
                525                 530                 535

CAC CAT CAC TAATCTAGA                                               1653
His His His
```

(2) INDICATIONS AS TO ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 539 amino acids

(B) KIND: amino acid

(D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1               5                  10                  15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
            20                  25                  30

Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
        35                  40                  45
```

Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
50 55 60

Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
65 70 75 80

Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
100 105 110

Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
130 135 140

Thr Pro Lys Leu Gly Gly Asp Ile Leu Leu Thr Gln Thr Pro Ala Ser
145 150 155 160

Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser
165 170 175

Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln
180 185 190

Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu
195 200 205

Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr
225 230 235 240

His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr
245 250 255

Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Ala Ala Gly Gly Pro Gly
260 265 270

Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
275 280 285

Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser
290 295 300

Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp
305 310 315 320

Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys
325 330 335

```
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala
            340                 345                 350

Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe
        355                 360                 365

Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met
    370                 375                 380

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr
385                 390                 395                 400

Thr Pro Lys Leu Gly Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ile
                405                 410                 415

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
            420                 425                 430

Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser
        435                 440                 445

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro
    450                 455                 460

Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
465                 470                 475                 480

Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
                485                 490                 495

Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn
            500                 505                 510

Arg Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln Lys Leu Ile Ser Glu
        515                 520                 525

Glu Asp Leu Asn Ser His His His His His His
    530                 535
```

(2) INDICATIONS AS TO ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) KIND: nucleotide

(C) STRAND TYPE: single strand

(D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TATATACTGC AGCTGCACCT GCGACCCTGG GCCACCAGCG GCCGCAGCAT CAGCCCG 57

(2) INDICATIONS AS TO ID NO: 6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) KIND: nucleotide
(C) STRAND TYPE: single strand
(D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CCGTGAATTC CAGGTGCAAC TGCAGCAGTC TGGGGCTGAA CTGGC 45

(2) INDICATIONS AS TO ID NO: 7:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) KIND: nucleotide
(C) STRAND TYPE: single strand
(D) TOPOLOGY: linear
(ii) KIND OF MOLECULE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGTCGACGTT AACCGACAAA CAACAGATAA AACG 34

(2) INDICATIONS AS TO ID NO: 8:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) KIND: nucleotide
(C) STRAND TYPE: single strand
(D) TOPOLOGY: linear
(ii) KIND OF MOLECULE: genome DNA
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(ix) FEATURE:
(A) NAME/KEY: CDS
(B) POSITION: 1..348
(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) POSITION: 1..348
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```
ATG AGA TTT CCT TCA ATT TTT ACT GCT GTT TTA TTC GCA GCA TCC TCC        48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 1               5                  10                  15

GCA TTA GCT GCT CCA GTC AAC ACT ACA ACA GAA GAT GAA ACG GCA CAA        96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

ATT CCG GCT GAA GCT GTC ATC GGT TAC TCA GAT TTA GAA GGG GAT TTC       144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

GAT GTT GCT GTT TTG CCA TTT TCC AAC AGC ACA AAT AAC GGG TTA TTG       192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

TTT ATA AAT ACT ACT ATT GCC AGC ATT GCT GCT AAA GAA GAA GGG GTA       240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

TCT CTC GAG AAA AGA GAG GCT GAA GCT GAA TTC CAG GTG CAA CTG CAG       288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Gln Val Gln Leu Gln
                85                  90                  95

CAG TCT GGG GCT GAA CTG GCA AGA CCT GGG GCC TCA GTG AAG ATG TCC       336
Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser
            100                 105                 110

TGC AAG GCT TCT                                                      348
Cys Lys Ala Ser
        115
```

2) INDICATIONS AS TO ID NO: 9:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) KIND: amino acid
(D) TOPOLOGY: linear
(ii) KIND OF MOLECULE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 1               5                  10                  15

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Gln Val Gln Leu Gln
                85                  90                  95

Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser
            100                 105                 110

Cys Lys Ala Ser
        115
```

(2) INDICATIONS AS TO ID NO: 10:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) KIND: nucleotide
(C) STRAND TYPE: single strand
(D) TOPOLOGY: linear
(ii) KIND OF MOLECULE: genome DNA

(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(ix) FEATURE:
(A) NAME/KEY: CDS
(B) POSITION: 1..354
(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) POSITION: 1..354
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

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ATG AGA TTT CCT TCA ATT TTT ACT GCT GTT TTA TTC GCA GCA TCC TCC        48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
  1               5                  10                  15

GCA TTA GCT GCT CCA GTC AAC ACT ACA ACA GAA GAT GAA ACG GCA CAA        96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

ATT CCG GCT GAA GCT GTC ATC GGT TAC TCA GAT TTA GAA GGG GAT TTC       144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45

GAT GTT GCT GTT TTG CCA TTT TCC AAC AGC ACA AAT AAC GGG TTA TTG       192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
    50                  55                  60

TTT ATA AAT ACT ACT ATT GCC AGC ATT GCT GCT AAA GAA GAA GGG GTA       240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65                  70                  75                  80

TCT CTC GAG AAA AGA GAG GCT GAA GCT GAA TTC ATG GCG CAG GTG CAA       288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Met Ala Gln Val Gln
                85                  90                  95

CTG CAG CAG TCT GGG GCT GAA CTG GCA AGA CCT GGG GCC TCA GTG AAG       336
Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
            100                 105                 110

ATG TCC TGC AAG GCT TCT                                              354
Met Ser Cys Lys Ala Ser
        115
```

2) INDICATIONS AS TO ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) KIND: amino acid

(D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
  1               5                  10                  15

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20                  25                  30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35                  40                  45
```

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
50 55 60

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65 70 75 80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Met Ala Gln Val Gln
85 90 95

Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
100 105 110

Met Ser Cys Lys Ala Ser
115

(2) INDICATIONS AS TO ID NO: 12:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) KIND: nucleotide
(C) STRAND TYPE: single strand
(D) TOPOLOGY: linear
(ii) KIND OF MOLECULE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TCACACAGAA TTCTTAGATC TATTAAAGAG GAGAAATTAA CC 42

(2) INDICATIONS AS TO ID NO: 13:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) KIND: nucleotide
(C) STRAND TYPE: single strand
(D) TOPOLOGY: linear
(ii) KIND OF MOLECULE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AGCACACGAT ATCACCGCCA AGCTTGGGTG TTGTTTTGGC 40

(2) INDICATIONS AS TO ID NO: 14:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) KIND: nucleotide
(C) STRAND TYPE: single strand
(D) TOPOLOGY: linear
(ii) KIND OF MOLECULE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

AGCACACAAG CTTGGCGGTG ATATCTTGCT CACCCAAACT CCA 43

(2) INDICATIONS AS TO ID NO: 15:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) KIND: nucleotide
(C) STRAND TYPE: single strand
(D) TOPOLOGY: linear
(ii) KIND OF MOLECULE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

AGCACACTCT AGAGACACAC AGATCTTTAG TGATGGTGAT GGTGATGTGA GTTTAGG 57

(2) INDICATIONS AS TO ID NO: 16:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) KIND: nucleotide
(C) STRAND TYPE: single strand
(D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CAGCCGGCCA TGGCGCAGGT GCAACTGCAG CAG 33

(2) INDICATIONS AS TO ID NO: 17:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) KIND: nucleotide
(C) STRAND TYPE: single strand
(D) TOPOLOGY: linear
(ii) KIND OF MOLECULE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TATATACTGC AGCTGCACCT GGCTACCACC ACCACCGGAG CCGCCACCAC CGCTACCACC 60

GCCGCCAGAA CCACCACCAC CAGCGGCCGC AGCATCAGCC CG 102

Official File: PCT/DE99/01350
Attorney's File: K 2675

**Amended Claims**

1. A multivalent $F_v$ antibody construct having at least four variable domains which are linked with one another via the peptide linkers 1, 2 and 3, wherein the peptide linkers 1 and 3 have 0 to 10 amino acids.

2. The $F_v$ antibody construct according to claim 1, wherein the peptide linkers 1 and 3 have the amino acid sequence GG.

3. The $F_v$ antibody construct according to claim 1 or 2, wherein the $F_v$ antibody construct is bivalent.

4. The $F_v$ antibody construct according to claim 3, wherein the peptide linker 2 has 11 to 20 amino acids.

5. The $F_v$ antibody construct according to claim 3 or 4, wherein the peptide linker 2 has the amino acid sequence $(G_4S)_4$.

6. The $F_v$ antibody construct according to claim 1 or 2, wherein the $F_v$ antibody construct is tetravalent.

7. The $F_v$ antibody construct according to claim 6, wherein the peptide linker 2 has 3 to 10 amino acids.

8. The $F_v$ antibody construct according to claim 6 or 7, wherein the peptide linker 2 comprises the amino acid sequence GGPGS.

9. The $F_v$ antibody construct according to any of claims 1 to 8, wherein the $F_v$ antibody construct is multispecific.

10. $F_v$ antibody construct according to claim 9, wherein the $F_v$ antibody construct is bispecific.

11. The $F_v$ antibody construct according to any of claims 1 to 8, wherein the $F_v$ antibody construct is monospecific.

12. A method of producing the multivalent $F_v$ antibody construct according to any of claims 1 to 11, wherein DNAs coding for the peptide linkers 1, 2 and 3 are ligated with DNAS coding for the four variable domains of an $F_v$ antibody construct such that the peptide linkers link the variable domains with one another and the resulting DNA molecule is expressed in an expression plasmid.

13. Expression plasmid coding for the multivalent $F_v$ antibody construct according to any of claims 1 to 11.

14. The expression plasmid according to claim 13, namely pDISC3x19-LL.

15. The expression plasmid according to claim 13, namely pDISC3x19-SL.

16. The expression plasmid according to claim 13, namely pPIC-DISC-LL.

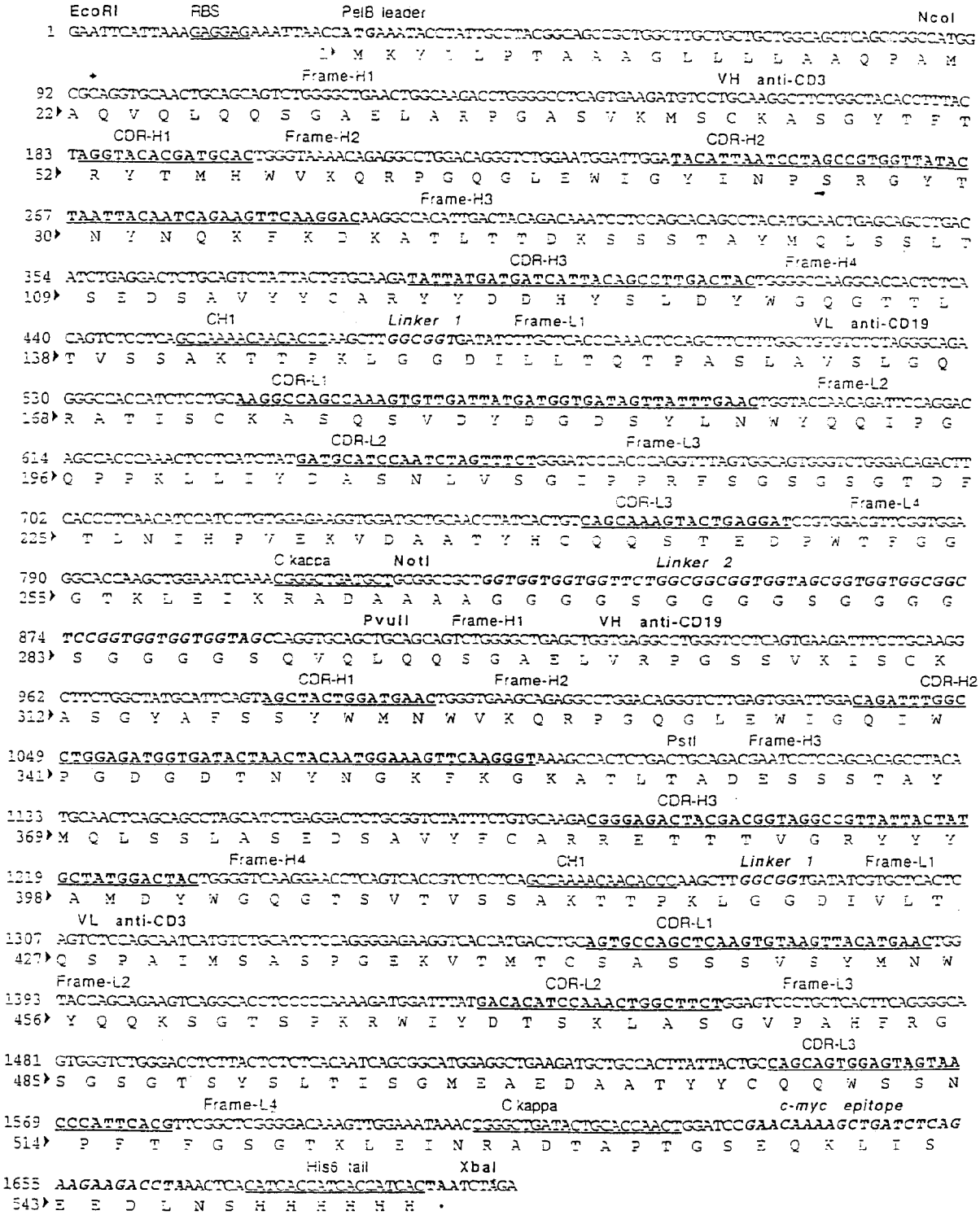
17. The expression plasmid according to claim 13, namely pPIC-DISC-SL.

18. The expression plasmid according to claim 13, namely pDISC5-LL.

19. The expression plasmid according to claim 13, namely pDISC6-SL.

20. Use of the multivalent $F_v$ antibody construct according to any of claims 1 to 11 for the diagnosis and/or treatment of diseases.

21. Use according to claim 20, wherein the diseases are viral, bacterial or tumoral diseases.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RBS
PelB leader
NcoI
Frame-H1
VH anti-CD3
CDR-H1
Frame-H2
CDR-H2
Frame-H3
CDR-H3
Frame-H4
CH1
Linker 1
Frame-L1
VL anti-CD19
CDR-L1
Frame-L2
CDR-L2
Frame-L3
CDR-L3
Frame-L4
C kappa
NotI
Linker 2
PvuII
Frame-H1
VH anti-CD19
CDR-H1
Frame-H2
CDR-H2
PstI
Frame-H3
CDR-H3
Frame-H4
CH1
Linker 1
Frame-L1
VL anti-CD3
CDR-L1
Frame-L2
CDR-L2
Frame-L3
CDR-L3
Frame-L4
C kappa
c-myc epitope
His6 tail
XbaI

FIGURE 5

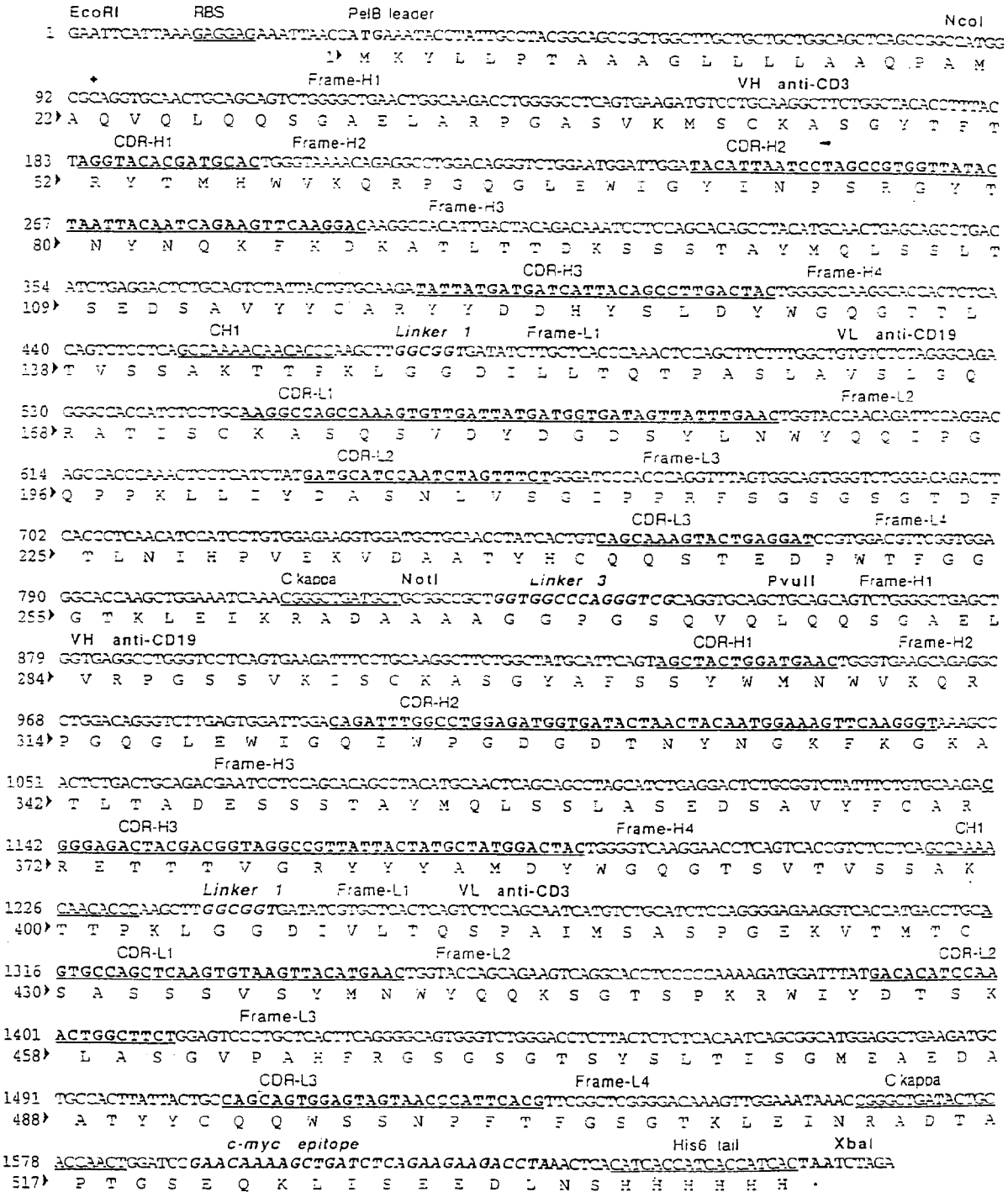
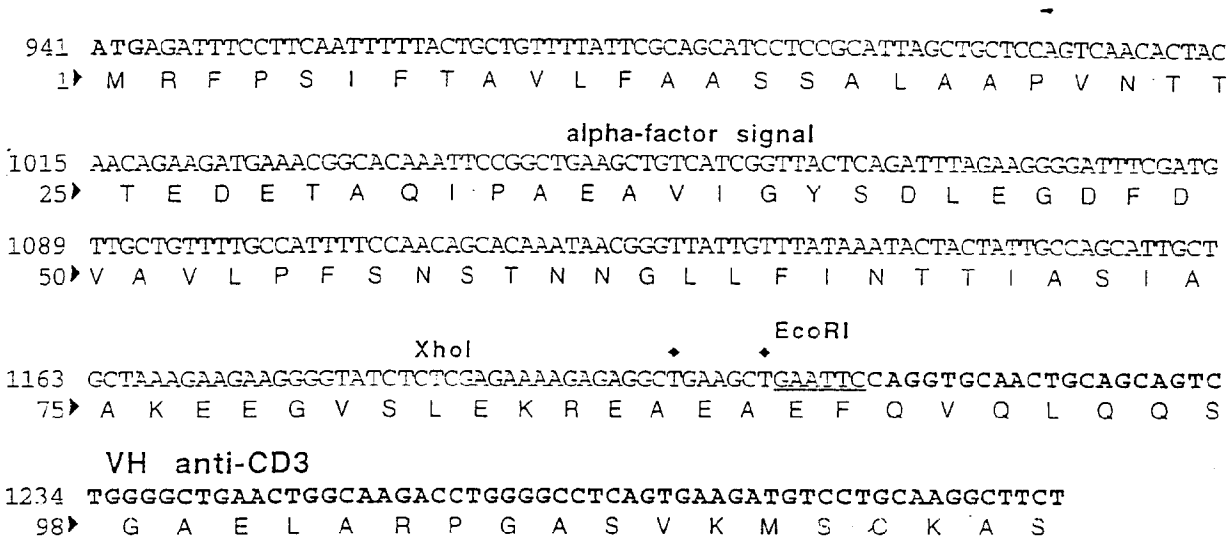

EcoRI
RBS
PelB leader
NcoI
Frame-H1
VH anti-CD3
CDR-H1
Frame-H2
CDR-H2
Frame-H3
CDR-H3
Frame-H4
CH1
Linker 1
Frame-L1
VL anti-CD19
CDR-L1
Frame-L2
CDR-L2
Frame-L3
CDR-L3
Frame-L4
Ckappa
NotI
Linker 3
PvuII
Frame-H1
VH anti-CD19
CDR-H1
Frame-H2
CDR-H2
Frame-H3
CDR-H3
Frame-H4
CH1
Linker 1
Frame-L1
VL anti-CD3
CDR-L1
Frame-L2
CDR-L2
Frame-L3
CDR-L3
Frame-L4
Ckappa
c-myc epitope
His6 tail
XbaI

FIGURE 6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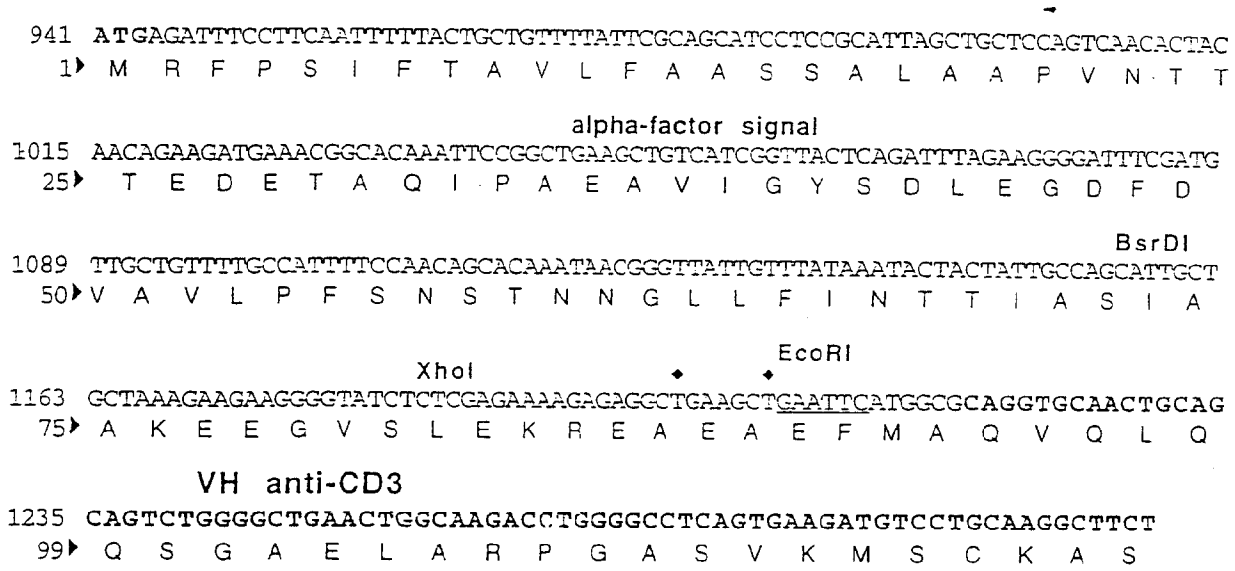
alpha-factor signal
1015 AACAGAAGATGAAACGGCACAAATTCCGGCTGAAGCTGTCATCGGTTACTCAGATTTAGAAGGGGATTTCGATG
25 T E D E T A Q I P A E A V I G Y S D L E G D F D
1089 TTGCTGTTTTTGCCATTTTCCAACAGCACAAATAACGGGTTATTGTTTATAAATACTACTATTGCCAGCATTGCT
50 V A V L P F S N S T N N G L L F I N T T I A S I A
XhoI
EcoRI
1163 GCTAAAGAAGAAGGGGTATCTCTCGAGAAAAGAGAGGCTGAAGCTGAATTCCAGGTGCAACTGCAGCAGTC
75 A K E E G V S L E K R E A E A E F Q V Q L Q Q S
VH anti-CD3
1234 TGGGGCTGAACTGGCAAGACCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCT
98 G A E L A R P G A S V K M S C K A S

FIGURE 7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alpha-factor signal
1015 AACAGAAGATGAAACGGCACAAATTCCGGCTGAAGCTGTCATCGGTTACTCAGATTTAGAAGGGGATTTCGATG
25 T E D E T A Q I P A E A V I G Y S D L E G D F D
BsrDI
1089 TTGCTGTTTTTGCCATTTTCCAACAGCACAAATAACGGGTTATTGTTTATAAATACTACTATTGCCAGCATTGCT
50 V A V L P F S N S T N N G L L F I N T T I A S I A
XhoI
EcoRI
1163 GCTAAAGAAGAAGGGGTATCTCTCGAGAAAAGAGAGGCTGAAGCTGAATTCATGGCGCAGGTGCAACTGCAG
75 A K E E G V S L E K R E A E A E F M A Q V Q L Q
VH anti-CD3
1235 CAGTCTGGGGCTGAACTGGCAAGACCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCT
99 Q S G A E L A R P G A S V K M S C K A S

FIGURE 8

UNSCANNABLE ITEM

RECEIVED WITH THIS APPLICATION

(ITEM ON THE 10TH FLOOR ZONE 5 IN THE FILE PREPARATION SECTION)

DOCUMENT REÇU AVEC CETTE DEMANDE

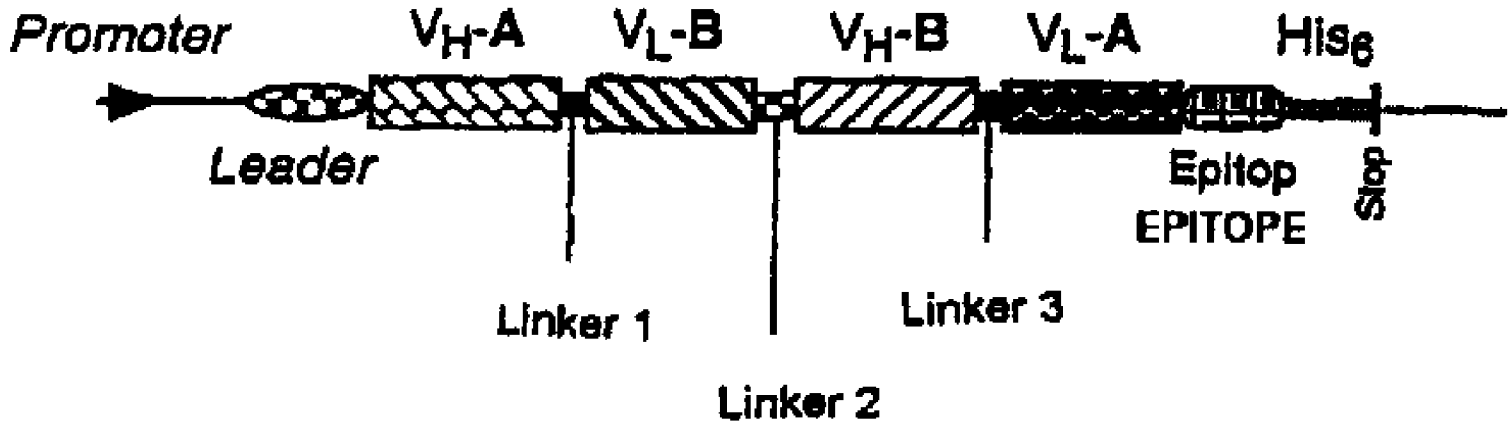
NE POUVANT ÊTRE BALAYÉ

(DOCUMENT AU 10 IÈME ÉTAGE AIRE 5 DANS LA SECTION DE LA

PRÉPARATION DES DOSSIERS)

P1-2-3-4-9-10

A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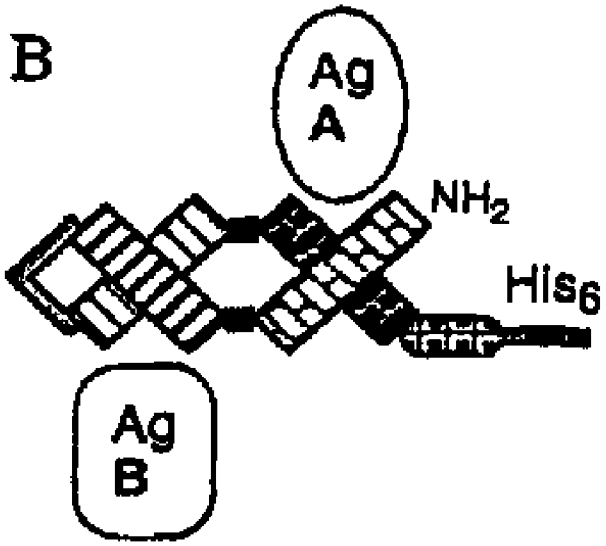
$V_L$-B
$V_H$-B
$V_L$-A
$His_6$
Leader
Epitop
EPITOPE
Stop
Linker 1
Linker 2
Linker 3

B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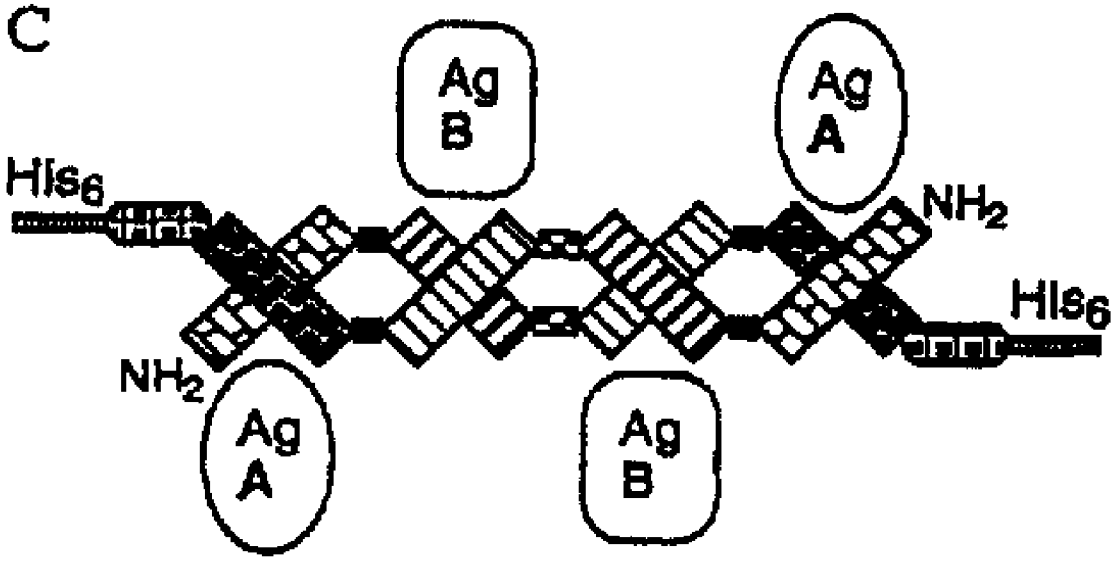
$NH_2$
$His_6$
Ag B

C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Ag A
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$NH_2$
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$NH_2$
Ag A
Ag B